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#3 03/13/01

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/742,684

DATE: 03/29/2001

TIME: 10:59:33

Input Set : N:\Crf3\RULE60\09742684.txt
Output Set: N:\CRF3\03292001\I742684.raw

ENTERED

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Mathews, Lawrence S.
6 Vale, Wylie W.
7 Tsuchida, Kunihiro
9 (ii) TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
10 RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
12 (iii) NUMBER OF SEQUENCES: 14
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
16 (B) STREET: 444 South Flower Street, Suite 2000
17 (C) CITY: Los Angeles
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 90071
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/742,684
C--> 30 (B) FILING DATE: 19-Dec-2000
31 (C) CLASSIFICATION:
48 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/476,123
35 (B) FILING DATE:
37 (A) APPLICATION NUMBER: US 08/300,584
38 (B) FILING DATE: 02-SEP-1994
41 (A) APPLICATION NUMBER: US 07/880,220
42 (B) FILING DATE: 08-MAY-1992
45 (A) APPLICATION NUMBER: US 07/773,229
46 (B) FILING DATE: 09-OCT-1991
49 (A) APPLICATION NUMBER: US 07/698,709
50 (B) FILING DATE: 10-MAY-1991
52 (viii) ATTORNEY/AGENT INFORMATION:
53 (A) NAME: Reiter, Stephen E.
54 (B) REGISTRATION NUMBER: 31,192
55 (C) REFERENCE/DOCKET NUMBER: P41 9927
57 (ix) TELECOMMUNICATION INFORMATION:
58 (A) TELEPHONE: 619-546-4737
59 (B) TELEFAX: 619-546-9392
62 (2) INFORMATION FOR SEQ ID NO: 1:
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 2563 base pairs
66 (B) TYPE: nucleic acid
67 (C) STRANDEDNESS: single

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68      (D) TOPOLOGY: linear
70      (ii) MOLECULE TYPE: cDNA
73      (ix) FEATURE:
74          (A) NAME/KEY: CDS
75          (B) LOCATION: 71..1609
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80      CTCCGAGGAA GACCCAGGGA ACTGGATATC TAGCGAGAAC TTCCTACGGC TTCTCCGGCG      60
82      CCTCGGGAAA ATG GGA GCT GCT GCA AAG TTG GCG TTC GCC GTC TTT CTT      109
83          Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu
84              1          5          10
86      ATC TCT TGC TCT TCA GGT GCT ATA CTT GGC AGA TCA GAA ACT CAG GAG      157
87      Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu
88          15          20          25
90      TGT CTT TTC TTT AAT GCT AAT TGG GAA AGA GAC AGA ACC AAC CAG ACT      205
91      Cys Leu Phe Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr
92          30          35          40          45
94      GGT GTT GAA CCT TGC TAT GGT GAT AAA GAT AAA CGG CGA CAT TGT TTT      253
95      Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe
96          50          55          60
98      GCT ACC TGG AAG AAT ATT TCT GGT TCC ATT GAA ATA GTG AAG CAA GGT      301
99      Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly
100          65          70          75
102      TGT TGG CTG GAT GAT ATC AAC TGC TAT GAC AGG ACT GAT TGT ATA GAA      349
103      Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu
104          80          85          90
106      AAA AAA GAC AGC CCT GAA GTG TAC TTT TGT TGC TGT GAG GGC AAT ATG      397
107      Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met
108          95          100          105
110      TGT AAT GAA AAG TTC TCT TAT TTT CCG GAG ATG GAA GTC ACA CAG CCC      445
111      Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro
112          110          115          120          125
114      ACT TCA AAT CCT GTT ACA CCG AAG CCA CCC TAT TAC AAC ATT CTG CTG      493
115      Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu
116          130          135          140
118      TAT TCC TTG GTA CCA CTA ATG TTA ATT GCA GGA ATT GTC ATT TGT GCA      541
119      Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala
120          145          150          155
122      TTT TGG GTG TAC AGA CAT CAC AAG ATG GCC TAC CCT CCT GTA CTT GTT      589
123      Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val
124          160          165          170
126      CCT ACT CAA GAC CCA GGA CCA CCC CCA CCT TCC CCA TTA CTA GGG TTG      637
127      Pro Thr Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu
128          175          180          185
130      AAG CCA TTG CAG CTG TTA GAA GTG AAA GCA AGG GGA AGA TTT GGT TGT      685
131      Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys
132          190          195          200          205
134      GTC TGG AAA GCC CAG TTG CTC AAT GAA TAT GTG GCT GTC AAA ATA TTT      733
135      Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe
136          210          215          220

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139	CCA	ATA	CAG	GAC	AAA	CAG	TCC	TGG	CAG	AAT	GAA	TAT	GAA	GTC	TAT	AGT	781
140	Pro	Ile	Gln	Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	
141				225					230					235			
143	CTA	CCT	GGA	ATG	AAG	CAT	GAG	AAC	ATA	CTA	CAG	TTC	ATT	GGT	GCA	GAG	829
144	Leu	Pro	Gly	Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	
145			240					245						250			
147	AAA	AGA	GGC	ACC	AGT	GTG	GAT	GTG	GAC	CTG	TGG	CTA	ATC	ACA	GCA	TTT	877
148	Lys	Arg	Gly	Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	
149		255					260						265				
151	CAT	GAA	AAG	GGC	TCA	CTG	TCA	GAC	TTT	CTT	AAG	GCT	AAT	GTG	GTC	TCT	925
152	His	Glu	Lys	Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	
153	270					275					280					285	
155	TGG	AAT	GAA	CTT	TGT	CAT	ATT	GCA	GAA	ACC	ATG	GCT	AGA	GGA	TTG	GCA	973
156	Trp	Asn	Glu	Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	
157				290						295					300		
159	TAT	TTA	CAT	GAG	GAT	ATA	CCT	GGC	TTA	AAA	GAT	GGC	CAC	AAG	CCT	GCA	1021
160	Tyr	Leu	His	Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	
161				305					310					315			
163	ATC	TCT	CAC	AGG	GAC	ATC	AAA	AGT	AAA	AAT	GTG	CTG	TTG	AAA	AAC	AAT	1069
164	Ile	Ser	His	Arg	Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	
165			320						325					330			
167	CTG	ACA	GCT	TGC	ATT	GCT	GAC	TTT	GGG	TTG	GCC	TTA	AAG	TTC	GAG	GCT	1117
168	Leu	Thr	Ala	Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	
169		335					340						345				
171	GGC	AAG	TCT	GCA	GGT	GAC	ACC	CAT	GGG	CAG	GTT	GGT	ACC	CGG	AGG	TAT	1165
172	Gly	Lys	Ser	Ala	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	
173	350					355					360					365	
175	ATG	GCT	CCA	GAG	GTG	TTG	GAG	GGT	GCT	ATA	AAC	TTC	CAA	AGG	GAC	GCA	1213
176	Met	Ala	Pro	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	
177				370						375					380		
179	TTT	CTG	AGG	ATA	GAT	ATG	TAC	GCC	ATG	GGA	TTA	GTC	CTA	TGG	GAA	TTG	1261
180	Phe	Leu	Arg	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	
181				385					390					395			
183	GCT	TCT	CGT	TGC	ACT	GCT	GCA	GAT	GGA	CCC	GTA	GAT	GAG	TAC	ATG	TTA	1309
184	Ala	Ser	Arg	Cys	Thr	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	
185			400						405					410			
187	CCA	TTT	GAG	GAA	GAA	ATT	GGC	CAG	CAT	CCA	TCT	CTT	GAA	GAT	ATG	CAG	1357
188	Pro	Phe	Glu	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Asp	Met	Gln	
189		415					420						425				
191	GAA	GTT	GTT	GTG	CAT	AAA	AAA	AAG	AGG	CCT	GTT	TTA	AGA	GAT	TAT	TGG	1405
192	Glu	Val	Val	Val	His	Lys	Lys	Lys	Arg	Pro	Val	Leu	Arg	Asp	Tyr	Trp	
193	430					435					440				445		
195	CAG	AAA	CAT	GCA	GGA	ATG	GCA	ATG	CTC	TGT	GAA	ACG	ATA	GAA	GAA	TGT	1453
196	Gln	Lys	His	Ala	Gly	Met	Ala	Met	Leu	Cys	Glu	Thr	Ile	Glu	Glu	Cys	
197				450						455				460			
199	TGG	GAT	CAT	GAT	GCA	GAA	GCC	AGG	TTA	TCA	GCT	GGA	TGT	GTA	GGT	GAA	1501
200	Trp	Asp	His	Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly	Cys	Val	Gly	Glu	
201				465					470					475			
203	AGA	ATT	ACT	CAG	ATG	CAA	AGA	CTA	ACA	AAT	ATC	ATT	ACT	ACA	GAG	GAC	1549

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204 Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp
205          480          485          490
207 ATT GTA ACA GTG GTC ACA ATG GTG ACA AAT GTT GAC TTT CCT CCC AAA      1597
208 Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys
209          495          500          505
211 GAA TCT AGT CTA TGATGGTGGC ACCGTCTGTA CACACTGAGG ACTGGGACTC      1649
212 Glu Ser Ser Leu
213 510
215 TGAAGTGGAG CTGCTAAGCT AAGGAAAGTG CTTAGTTGAT TTTCTGTGTG AAATGAGTAG      1709
217 GATGCCTCCA GGACATGTAC GCAAGCAGCC CCTTGTGGAA AGCATGGATC TGGGAGATGG      1769
219 ATCTGGGAAA CTTACTGCAT CGTCTGCAGC ACAGATATGA AGAGGAGTCT AAGGGAAAAG      1829
221 CTGCAAACTG TAAAGAACTT CTGAAAATGT ACTCGAAGAA TGTGGCCCTC TCCAAATCAA      1889
223 GGATCTTTTG GACCTGGCTA ATCAAGTATT TGCAAAACTG ACATCAGATT TCTTAATGTC      1949
225 TGTCAGAAGA CACTAATTCC TTAAATGAAC TACTGCTATT TTTTAAAT GAAAACTTT      2009
227 TCATTTTCAGA TTTTAAAAAG GGTAACTTT TATTGCATT TCTGTGTTT CTATAAATGA      2069
229 CTATTGTAAT GCCAACATGA CACAGCTTGT GAATGTGTAG TGTGCTGCTG TTCTGTGTAC      2129
231 ATAGTCATCA AAGTGGGGTA CAGTAAAGAG GCTTCCAAGC ATTACTTTAA CCTCCCTCAA      2189
233 CAAGGTATAC CTCAGTTCCA CGGTTGTAA ATTATAAAAT TGAAAAACACT AACAGAAATTT      2249
235 GAATAAATCA GTCCATGTTT TATAACAAGG TTAATTACAA ATTCAGTGTG TTATTTAAGA      2309
237 AAAAATGGTA AGCTATGCTT AGTGCCAATA GTAAGTGGCT ATTTGTAAAG CAGTGTTTAA      2369
239 GCTTTTCTTC TACTGGCTTG TAATTTAGGG AAAACAAGTG CTGTCTTTGA AATGGAAAAG      2429
241 AATATGGTGT CACCCTACCC CCCATACTTA TATCAAGGTC CCAAAATATT CTTTCCATT      2489
243 TCAAAGACAG CACTTTGAAA ACCCTAAATT ACAAGCCAGT AGAAGAAAAG CTAAACACG      2549
245 CTTTACAAAT AGCC      2563
248 (2) INFORMATION FOR SEQ ID NO: 2:
250 (i) SEQUENCE CHARACTERISTICS:
251 (A) LENGTH: 513 amino acids
252 (B) TYPE: amino acid
253 (D) TOPOLOGY: linear
255 (ii) MOLECULE TYPE: protein
257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
259 Met Gly Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
260 1 5 10 15
262 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
263 20 25 30
265 Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr Gly Val Glu
266 35 40 45
268 Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
269 50 55 60
271 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
272 65 70 75 80
274 Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu Lys Lys Asp
275 85 90 95
277 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
278 100 105 110
280 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
281 115 120 125
283 Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
284 130 135 140

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286 Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
287 145 150 155 160
289 Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
290 165 170 175
292 Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
293 180 185 190
295 Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
296 195 200 205
298 Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
299 210 215 220
301 Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
302 225 230 235 240
304 Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
305 245 250 255
307 Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
308 260 265 270
310 Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
311 275 280 285
313 Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
314 290 295 300
316 Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
317 305 310 315 320
319 Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
320 325 330 335
322 Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
323 340 345 350
324 Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
325 355 360 365
327 Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
328 370 375 380
330 Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
331 385 390 395 400
333 Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
334 405 410 415
336 Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
337 420 425 430
340 Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
341 435 440 445
343 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
344 450 455 460
346 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
347 465 470 475 480
349 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
350 485 490 495
352 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
353 500 505 510
355 Leu
358 (2) INFORMATION FOR SEQ ID NO: 3:
360 (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09742684.txt

Output Set: N:\CRF3\03292001\I742684.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10